

CCL27, CCL28, CCL3, COL3A1, COL4A1, COL4A3, CSSF1, CSF2, CSF3, CTGF, CX3CL1, CXCL1, CXCL10, CXCL11, CXCL12, FGF10, FGF11, FGF12, FGF13, FGF17, FGF2, FGF3, FGF5, FGF7, FGF8, FGF9, FGF, IFNG, IGF1, IGF2, IGFBP1, IGFBP2, IGFBP3, IGFBP4, IGFBP5, IGFBP6, IGFBP7, IL10, IL11, IL6, IL7, IL8, IL9, ITGA5, ITGAL, ITGAM, ITGB2, KDR, KITLG, LBP, LTA, MMP7, MMP8, MMP9, MPO, NCAM2, NFKB1, NFKB2, NOS2A, OSMR, PDGFA, PDGFB, PECAM1, SMAD6, SMAD7, SOCS1, SOCS3, SOCS5, STAT3, TEK, TGFA, TGFB1, TGFB2, TGFB3, TGFB1, DCL2L2, BMP1, BMP15, BMP5, BMP3, BMP4, BMP5, BMP6, BMP7, BMP8A, BMP8B, CALCA, CALCB, CAV1, CCL4, CCL4L1, CCL4L2, CCL5, CCL7, CD14, CD4, CD40, CD40LG, CD83, CD8A, CD8B, COL18A1, COL1A1, CXCL13, CXCL2, CXCL5, CXCL9, ECGF1, EDN1, EGF, EGR1, EPO, FADD, FAS, FGF1, FLT1, FN1, GAPDH, GDF3, GDF5, MSTN, GDF9, HGF, HMGB1, IAPP, ICAM2, IFNB1, IL12A, IL13, IL15, IL16, IL17A, IL18, IL1A, IL1B, IL2, IL3, IL4, IL5, MAPK14, MET, MMP1, MMP10, MMP11, MMP12, MMP13, MMP14, MMP15, MMP2, MMP24, MMP3, PF4, PLA2G4A, PTGS1, PTGS2, SELE, SELP, SERPINE1, SLPI, SMAD1, SMAD2, SMAD3, SMAD4, TIE1, TIMP1, TIMP2, TIMP3, TNC, TNF, TNFSF10, VCAM1, VEGFB, VEGFC, XCL1, XCL2.

**29.** The method according to claim **23**, wherein the clinical parameters further include Injury Severity Score (ISS), Acute Physiology and Chronic Health Evaluation II (APACHE-II) scores, wound size, and associated vascular injury.

**30.** A method for determining a patient-specific probability of disease, the disease including at least one of malignancy in a thyroid nodule, transplant glomerulopathy, impaired wound healing, and breast cancer, said method including:

- collecting clinical parameters from a plurality of patients to create a training database, the clinical parameters including at least one of fine needle aspiration biopsy results, ultrasound data, lymph node size, imaging data, Gail model cutoff, mammogram results, MRI results, breast size, personal history of breast disease, and biomarker levels from at least one of serum, wound effluent and biopsy tissue, the biomarker levels including gene expression levels for an IP-10 gene, IL-6 gene, MCP-1 gene, IL-5 gene, and RANTES gene;

- creating a fully unsupervised Bayesian Belief Network model using data from the training database;

- validating the fully unsupervised Bayesian Belief Network model;

- collecting the clinical parameters for an individual patient;
- receiving the clinical parameters for the individual patient into the fully unsupervised Bayesian Belief Network model;

- outputting the patient-specific probability of disease from the fully unsupervised Bayesian Belief Network model to a graphical user interface for use by a clinician; and
- updating the fully unsupervised Bayesian Belief Network model using the clinical parameters for the individual patient and the patient-specific probability of disease.

**31.** The method according to claim **30**, wherein the imaging data includes results from electrical impedance scanning, wherein the results from the electrical impedance scanning include a definitely benign score, probably benign score, suspicious for cancer score, probably cancer score, and definitely cancer score,

wherein the fine needle aspiration biopsy results include an inadequate score, indeterminate score, negative score, and positive score,

wherein the ultrasound data include a complex cyst score, mixed score, simple cyst score, and solid score, and wherein the lymph node size includes a less than 18 centimeters score, 18-31 centimeters score, and greater than 31 centimeters score.

**32.** The method according to claim **30**, wherein said creating of the fully unsupervised Bayesian Belief Network model includes creating the fully unsupervised Bayesian Belief Network model without human-developed decision support rules.

**33.** The method according to claim **30**, further including estimating an accuracy of the patient-specific probability of disease, the accuracy including at least one of model sensitivity, model specificity, positive and negative predictive values, and overall accuracy.

**34.** The method according to claim **30**, wherein the clinical parameters further include functional status of the thyroid nodule, number of cervical lymph nodes, serum thyrotropin level, pre-operative diagnosis, nuclear medicine rating, age, and ethnicity.

**35.** The method according to claim **34**, wherein:

- the pre-operative diagnosis is usable to estimate the fine needle aspiration biopsy results,

- the nuclear medicine rating is usable to estimate the lymph node size, imaging data, and the age,

- the age is usable to estimate the nuclear medicine rating and imaging data,

- the functional status of the thyroid nodule is usable to estimate the age,

- the number of cervical lymph nodes is usable to estimate the imaging data, and

- the ethnicity is usable to estimate the number of cervical lymph nodes.

**36.** The method according to claim **30**, wherein the biomarker levels include gene expression levels for an ICAM-1 gene, IL-10 gene, CCL-3 gene, CD-86 gene, CCL-2 gene, CXCL-11 gene, CD-80 gene, GNLY gene, PRF-1 gene, CD40LG gene, IFNG gene, CD-28 gene, CXCL-10 gene, CCR-5 gene, CD-40 gene, CTLA-4 gene, TNF gene, CXCL-9 gene, CX3CR-1 gene, FOXP-3 gene, EDN-1 gene, CD-4 gene, TBX-21 gene, FASLG gene, C-3 gene, CD3E gene, CXCR-3 gene, and CCL-5 gene.

**37.** The method according to claim **36**, wherein:

- the gene expression level for the CD-86 gene is usable to estimate the gene expression level for the CCL-3 gene,

- the gene expression levels for the CCL-2 gene, the CD40LG gene and the CXCL11 gene are usable to estimate the gene expression level for the CD-86 gene,

- the gene expression level for the PRF-1 gene is usable to estimate the gene expression level for the GNLY gene,

- the gene expression levels for the GNLY gene and the CXCL-10 gene are usable to estimate the gene expression level for the CD-80 gene,

- the gene expression level for the CD-80 gene is usable to estimate the gene expression level for the CXCL-11 gene,

- the gene expression levels for the IFNG gene and the CD-28 gene are usable to estimate the gene expression level for the CD40LG gene,

- the gene expression level for the CCR-5 gene is usable to estimate the gene expression level for the PRF-1 gene,